

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 18, 2001, 15:57:52 ; Search time 31.07 Seconds
(without alignments)
3253.332 Million cell updates/sec

Title: US-09-587-111-5

Perfect score: 4004
Sequence: 1 MTSPPSSPVFLRLTLDGGE.....EDEDGASENNVYPVOLLGSLN 764

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: SPTRMBL_16:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_organalle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4004	100.0	764	4 Q9Y5S1	Q9Y5S1 homo sapien
2	3945	98.5	764	4 Q9Y670	Q9Y670 homo sapien
3	3159	78.9	756	11 Q9WTR1	Q9WTR1 mus musculu
4	3051.5	76.2	761	11 Q9WTR2	Q9WTR2 mus musculu
5	3041.5	76.0	761	11 Q9WTR3	Q9WTR3 mus musculu
6	3028.5	75.6	762	11 Q9WTR4	Q9WTR4 mus musculu
7	1652	41.3	838	11 Q9JMS7	Q9JMS7 ratu
8	1652	41.3	838	11 Q9JMS8	Q9JMS8 ratu
9	1651.5	41.2	839	4 Q9H304	Q9H304 homo sapien
10	1648.5	41.2	839	4 Q9H305	Q9H305 homo sapien
11	1644.5	41.1	839	4 Q9H306	Q9H306 homo sapien
12	1636.5	40.9	839	4 Q9H307	Q9H307 homo sapien
13	1467	36.6	871	4 Q9H308	Q9H308 homo sapien
14	1467	36.6	871	4 Q9H309	Q9H309 homo sapien
15	1465.5	36.6	871	4 Q9H310	Q9H310 homo sapien
16	1464	36.6	871	4 Q9H311	Q9H311 homo sapien
17	1458.5	36.4	871	11 Q9H312	Q9H312 mus musculu
18	1457.5	36.4	871	11 Q9H313	Q9H313 mus musculu
19	1452.5	36.3	871	11 Q9H314	Q9H314 mus musculu

20	1446.5	36.1	873	11 Q9H315	Q9H315 mus musculu
21	1442.5	36.0	778	11 Q9H316	Q9H316 mus musculu
22	1112.5	27.8	528	11 Q9H317	Q9H317 mus musculu
23	969	24.2	511	4 Q9H318	Q9H318 mus musculu
24	933	23.3	471	11 Q9H319	Q9H319 mus musculu
25	634	15.8	725	4 Q9H320	Q9H320 mus musculu
26	631	15.8	725	4 Q9H321	Q9H321 mus musculu
27	630	15.7	725	4 Q9H322	Q9H322 mus musculu
28	607.5	15.2	727	11 Q9H323	Q9H323 mus musculu
29	589	14.7	723	11 Q9H324	Q9H324 mus musculu
30	586	14.6	730	6 Q9H325	Q9H325 mus musculu
31	584	14.6	723	11 Q9H326	Q9H326 mus musculu
32	579.5	14.5	729	4 Q9H327	Q9H327 mus musculu
33	469.5	11.7	769	5 Q9H328	Q9H328 mus musculu
34	440.5	11.0	729	11 Q9H329	Q9H329 mus musculu
35	428.5	10.7	750	5 Q9H330	Q9H330 mus musculu
36	414	10.3	900	5 Q9H331	Q9H331 mus musculu
37	392.5	9.8	790	5 Q9H332	Q9H332 mus musculu
38	364	9.1	937	5 Q9H333	Q9H333 mus musculu
39	338	8.4	1123	5 Q9H334	Q9H334 mus musculu
40	261	6.5	519	5 Q9H335	Q9H335 mus musculu
41	255	6.4	1913	5 Q9H336	Q9H336 mus musculu
42	233	5.8	904	5 Q9H337	Q9H337 mus musculu
43	229	5.7	1453	5 Q9H338	Q9H338 mus musculu
44	226.5	5.7	981	6 Q9H339	Q9H339 mus musculu
45	224.5	5.6	890	11 Q9H340	Q9H340 mus musculu

ALIGNMENTS

RESULT 1
ID Q9Y5S1 PRELIMINARY: PRT: 764 AA.

AC Q9Y5S1; 01-NOV-1999 (TREMUR1.12, Created)
DT 01-NOV-1999 (TREMUR1.12, Last sequence update)
DT 01-MAR-2001 (TREMUR1.16, Last annotation update)
DE VANILLOID RECEPTOR-LIKE PROTEIN 1.
GN VR-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99215558; PubMed-10201375;
RA Caterina M.J., Rosen T.A., Tomlinaga M., Brake A.J., Julius D.;
RT "A capsaicin-receptor homologue with a high threshold for noxious
heat";
RT Nature 398:436-441(1999).
RL EMBL: AF129112; AAD26363.1; -
DR InterPro: IPR002110; -
DR InterPro: IPR002111; -
DR Pfam: PF00023; ank; 3.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR SMART: SM00248; ANK; 1.
KW Receptor.
SQ SEQUENCE 764 AA; 85980 MW; A73E3696E70F91E9 CRC64;

Query Match 100.0%; Score 4004; DB 4; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPPSSPVFLRLTLDGGESEADRGKLPFMSQFQEGEDRKRFAPQIRVNLNY 60
DB 1 MTSPPSSPVFLRLTLDGGESEADRGKLPFMSQFQEGEDRKRFAPQIRVNLNY 60
QY 61 RKGTCASQPDNRRDRDLFNAVSKGVPEDLAQLPEYLSKTSKYLTDSEYEGSGTKTCL 120
DB 61 RKGTCASQPDNRRDRDLFNAVSKGVPEDLAQLPEYLSKTSKYLTDSEYEGSGTKTCL 120

QY	121	MAKVALNKDGNVACITLPLTLOIDRSGNPOPLVNAQCDDYVYRGSHALHIEKRSLQCV	180
Db	121	MKAVLNLKDGYNACITLPLTLOIDRSGNPOPLVNAQCDDYVYRGSHALHIEKRSLQCV	180
QY	181	LLVENGAVNVARACGREFQKQGTCTCFYEGELPLSLAACKTQMDVSVYLLENPHQPSLQA	240
Db	181	LLVENGAVNVARACGREFQKQGTCTCFYEGELPLSLAACKTQMDVSVYLLENPHQPSLQA	240
QY	241	TDGSGNTVYLAHVMISGNSAENALVYSMTDGLLQAGARLCIPVVOLEDINLODLPPLK	300
Db	241	TDGSGNTVYLAHVMISGNSAENALVYSMTDGLLQAGARLCIPVVOLEDINLODLPPLK	300
QY	301	AAKGGKIEIFPHILIIQREFSGLSLRSKFTFMCYCPVAVSVLYDLASVDSCEENSVLETIAP	360
Db	301	AAKGGKIEIFPHILIIQREFSGLSLRSKFTFMCYCPVAVSVLYDLASVDSCEENSVLETIAP	360
QY	361	HCKSPHRRHRYVLEPLNKLLOAKMDLLIPKFFLNLCLNYMFIFTAVAYHOPLTKKQA	420
Db	361	HCKSPHRRHRYVLEPLNKLLOAKMDLLIPKFFLNLCLNYMFIFTAVAYHOPLTKKQA	420
QY	421	PHLKAEGNSMLLGHILLILGGITYLLVGLQWYWRHRYVLEMTSFDSYFEILLFLFOALL	480
Db	421	PHLKAEGNSMLLGHILLILGGITYLLVGLQWYWRHRYVLEMTSFDSYFEILLFLFOALL	480
QY	481	TVVSQVLCFLAIEMYLPLTVLSATVLGMNLNLYYTRGROHGIYSVMIOKLYILDLLEFL	540
Db	481	TVVSQVLCFLAIEMYLPLTVLSATVLGMNLNLYYTRGROHGIYSVMIOKLYILDLLEFL	540
QY	541	ILYVFLGFAVALVSLSOGAARPPAPGPNNATESVOPMEQOEDBGNGAOYRGLLEASLEL	600
Db	541	ILYVFLGFAVALVSLSOGAARPPAPGPNNATESVOPMEQOEDBGNGAOYRGLLEASLEL	600
QY	601	FKFTTGMGELAFQOLHPRGVLLLLLAAYLVLTITLNLNLMSFTVNSVATDSMSIW	660
Db	601	FKFTTGMGELAFQOLHPRGVLLLLLAAYLVLTITLNLNLMSFTVNSVATDSMSIW	660
QY	661	KLOKRAISYLEMENGYWMCRRKQORAGVNLVGTGKDGSSPDERMCFRVEEVMASMEQTLPT	720
Db	661	KLOKRAISYLEMENGYWMCRRKQORAGVNLVGTGKDGSSPDERMCFRVEEVMASMEQTLPT	720
QY	721	LCEDPSGAGVPRTELENVYLASPPKEDBDGASEENVYVOLLQSN	764
Db	721	LCEDPSGAGVPRTELENVYLASPPKEDBDGASEENVYVOLLQSN	764
RESULT 2			
ID	Q9Y670	PRELIMINARY	PRT; 764 AA.
AC	Q9Y670		
DT	01-NOV-1999 (TReMBLrel. 12, Created)		
DT	01-NOV-1999 (TReMBLrel. 12, Last sequence update)		
DT	01-MAR-2001 (TReMBLrel. 16, last annotation update)		
DE	VANILLOID RECEPTOR-LIKE PROTEIN.		
CN	VRL.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	SEQUENCE FROM N.A.		
RP	Garcia R.L., Delmas P., Cesare P., England S., Liapi A., Wood J.N.;		
RA	"Cloning and functional expression of VRL, a vanilloid receptor-like		
RT	gene";		
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF103906; AAD41724.1; -.		
DR	InterPro; IPR002110; -.		
DR	InterPro; IPR002111; -.		
DR	Pfam; PF00023; ank. 3.		
DR	PROSITE; PSS0088; ANK_REPEAT. 1.		
DR	PROSITE; PSS0297; ANK_REPEAT_REGION. 1.		
DR	SMART; SM00248; ANK. 1.		
DR	Receptor.		

Seq	Sequence	764 AA;	86053 MM;	AF9DEB8F495EBE43A0 CRC64;
QY	Query Match	98.5%;	Score 3945;	DB 4; Length 764;
	Best Local Similarity	98.2%;	Pred. No. 0;	
	Matches 750; Conservative	6; Mismatches	8; Indels	0; Gaps
QY	1	MTSPSSSPVFLETLTDGQEDGSEADNRKLPFGSGLPFMESOFQGEDRKFAPOJRVNLNT	60	
Db	1	MTSPSSSPVFLETLTDGQEDGSEADNRKLPFGSGLPFMESOFQGEDRKFAPOJRVNLNT	60	
QY	61	RKGTGASQPDENRRDRDLFNVAVSRGVEDLAGLPEYLSKTSKTLTDSYEGSGTGKTC	120	
Db	61	RKGTGASQPDENRRDRDLFNVAVSRGVEDLAGLPEYLSKTSKTLTDSYEGSGTGKTC	120	
QY	121	MKAVLNTKDGVNACCLPLLOIDRDSGNQOPVYNNQCTDDYRGHSALHAIATEKSLQCVK	180	
Db	121	MKAVLNTKDGVNACCLPLLOIDRDSGNQOPVYNNQCTDDYRGHSALHAIATEKSLQCVK	180	
QY	181	LLVENGANVAARACGREFQKQGTCEYFGEPLPLSLAATKQMDVSYLLENPHOPASLOA	240	
Db	181	LLVENGANVAARACGREFQKQGTCEYFGEPLPLSLAATKQMDVSYLLENPHOPASLOA	240	
QY	241	TDSGNVTYLAHLYMISDASENIALYTSMTYGLLOAGARLCPVQLEDIRLQDITPLKTL	300	
Db	241	TDSGNVTYLAHLYMISDASENIALYTSMTYGLLOAGARLCPVQLEDIRLQDITPLKTL	300	
QY	301	AAKGKIEIFRHIIQREBSGLSHLSRKTEEMCYPVVRSLDLSVDSCEENSVLEITAF	360	
Db	301	AAKGKIEIFRHIIQREBSGLSHLSRKTEEMCYPVVRSLDLSVDSCEENSVLEITAF	360	
QY	361	HCKSPHRRHVVLEPLNKLQAKMDLIPKFFLFLCNLYMFTFAVAYHQPLKKQAA	420	
Db	361	HCKSPHRRHVVLEPLNKLQAKMDLIPKFFLFLCNLYMFTFAVAYHQPLKKQAA	420	
QY	421	PLKAEVNSMLTGHTLILGGLYLVGQVYFMRHVFIMISFIDYFEILFLEFOALL	480	
Db	421	PLKAEVNSMLTGHTLILGGLYLVGQVYFMRHVFIMISFIDYFEILFLEFOALL	480	
QY	481	TVVSQVLCFLAIEWLPLLVSAVLYGWLNLTYTRGFQHTGISYVMIQKVLRLDLRELL	540	
Db	481	TVVSQVLCFLAIEWLPLLVSAVLYGWLNLTYTRGFQHTGISYVMIQKVLRLDMVRELV	540	
QY	541	TYLVPLFCFAALVSLSGEAPRAPCPNATSEVQOPMEGDESGNAGVYGGIIEASIEL	600	
Db	541	TYLVPLFCFAALVSLSGEAPRAPCPNATSEVQOPMEGDESGNAGVYGGIIEASIEL	600	
QY	601	EKFTIGMELFQOQLHFRGVYLLLLLAIVLLTYLLNLMLALMSETVNSVATDSMSIW	660	
Db	601	EKFTIGMELFQOQLHFRGVYLLLLLAIVLLTYLLNLMLALMSETVNSVATDSMSIW	660	
QY	661	KLGKAIISVLEENGYWMCRRKQKQAGVYMLTVYTRKDGSDERWCRRVEVYNNASWEOQLPT	720	
Db	661	KLGKAIISVLEENGYWMCRRKQKQAGVYMLTVYTRKDGSDERWCRRVEVYNNASWEOQLPT	720	
QY	721	LCBPSGAGVPTLENPYLASPKEDEGASSEENVVPOLLQSN	764	
Db	721	LCBPSGAGVPTLENPYLASPKEDEGASSEENVVPOLLQSN	764	
RESULT	3			
Q9WTR1	PRELIMINARY;	PRT;	756 AA.	
AC	O9WTR1;			
DT	01-NOV-1999 (Tremblere1.12, Created)			
DT	01-NOV-1999 (Tremblere1.12, Last sequence update)			
DT	01-MAR-2001 (Tremblere1.16, Last annotation update)			
DE	GROWTH FACTOR REGULATED CALCIUM CHANNEL.			
GN	VR1 OR GRC.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI	TaxID=10090;			

[1]
RN SEQUENCE FROM N.A.
RP STRAIN-C57 BLACK-6; TISSUE=SPLEEN;
RA Kanazaki M., Zhang Y., Kojima I.;
RT "growth factor regulated calcium channel."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB021665; BAA78478.1; -
DR MGD: MGI:1341836; Vrl1.
DR InterPro: IPR002110; -
DR InterPro: IPR002111; -
DR Pfam: PF00023; ank; 3.
DR PROSITE: PSS0088; ANK_REPEAT; 1.
DR PROSITE: PSS0297; ANK_REPEAT_REGION; 1.
DR SMART: SM00248; ANK; 1.
SQ SEQUENCE 756 AA; 85964 MW; 4C037D0F6066EFAC CRC64;

Query Match 78.9%; Score 3159; DB 11; Length 756;
Best Local Similarity 80.3%; Pred. No. 7.2e-241;
Matches 615; Conservative 55; Mismatches 84; Indels 12; Gaps 5;

QY 1 MTSSSSPVFLFETLDGQEDGSEADGKLDPGSGLPMEQFQGEDRKFPQIRVNLNY 60
DB 1 MTSASNPAPFLFETSDGDEGSAEVNKGK---NEPPMESPFQGEDRNFSPOIKVNLNY 56
QY 61 RKGASQDPDRFRDRDLFNAVSRGVPEDLAIPYLSTKSKYLTDESEYEGSTGKTCL 120
DB 57 RKGAGPQDQDNRDRDRLEFVSRCVPEELTGLEYLRKSKYLTDSAYTEGSTGKTCL 116
QY 121 MKAVNLKQGVNACILPLQIDRDSGNPQPLVNAOCTDDYRGSHALHIAIEKRSLOCVK 180
DB 117 MKAVNLQDQGVNACILPLQIDRDSGNPQPLVNAOCTDEYRGSHALHIAIEKRSIMCVK 176
QY 181 LTVNGANVHARACGRPFQKQGTCEYFGEPLSLAACKTQMDVSYLLENPHOPASIQ 240
DB 177 LTVNGANVHARACGRPFQKQGTCEYFGEPLSLAACKTQMDVSYLLENPHOPASILEA 236
QY 241 TDSQGNVTHALVMIISDNSAENIALVTSMDGLQAGARLCPVQLEDIRNLQDITPLKL 300
DB 237 TDSIGNVTHALVMIADNSPENSALVIMYDSLLQMGARLCPVQLEDICHHQGITPLKL 296
QY 301 AAKGKTEIFRHLQREFSGT-SHLSRKFTWCYGVAVRSLYDLASVDSCEENVLEIIA 359
DB 297 AAKGKTEIFRHLQREFSGT-SHLSRKFTWCYGVAVRSLYDLASVDSCEENVLEIIA 356
QY 360 FHCSPIRHRMVLEPLNKLQAKWDLIPKFLNFCNLVYMFTRAVAHOPITKQ 419
DB 357 FHCSPIRHRMVLEPLNKLQAKWDLIPKFLNFCNLVYMFTRAVAHOPITKQ 416
QY 420 APHLKAEGNSMLTGHLLILGILYLLVQGLWFMRRHVFIMISFIDSEIFELFOAL 479
DB 417 IPSSKAFQSGDMLLGHLLILGILYLLVQGLWFMRRHVFIMISFIDSEIFELFOAL 476
QY 480 LTVVSOVLCFLAIETWYLPPLVSALVGLWNLVYTRGFQHTGITSVMIOKVILRDLEFL 539
DB 477 LTVLSOVLRFETEMWYLPPLVSSLVGLWNLVYTRGFQHTGITSVMIOKVILRDLEFL 536
QY 540 LTVVPLFEGFVALVSLDSOAMRBEAPRTGPNATESVQPMQOEDGEGNAQVRGIIASLE 599
DB 537 LTVVPLFEGFVALVSLDSOAMRBEAPRTGPNATESVQPMQOEDGEGNAQVRGIIASLE 594
QY 600 LKFTTIGMGLAFQEOHIFRGVLLLLAVLVLYIILNMLIALMSETVSVATDSISI 659
DB 595 LKFTTIGMGLAFQEOHIFRGVLLLLAVLVLYIILNMLIALMSETVSVATDSISI 654
QY 660 WKLOKAIASVLEMENGYWMCRRKQ-RAGVMLTVGTRKPDGSPDERKCFRVEEVNMAWQOTL 718
DB 655 WKLOKAIASVLEMENGYWMCRRKRRHAGRLKVGTRKGDIPDERKCFRVEEVNMAWQOTL 714
QY 719 PTLCEPDSGAGVPTLENPVLASPKKEDEGASBENVVYVOLLQSN 764
DB 715 PTLSEDPGAGITGYKKNP-----SKPEKNSASEBDHPLQVLOSH 756

RESULT 4
ID 09WMD2 PRELIMINARY; PRT: 761 AA.
AC 09WMD2;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE VANILLOID RECEPTOR-LIKE PROTEIN 1.
GN VRL-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=99215558; PubMed=10201375;
RA Caterina M.J., Rosen T.A., Tominaga M., Brake A.J., Julius D.;
RT "A capsaicin-receptor homologue with a high threshold for noxious
heat".
RL Nature 398:436-441(1999).
DR EMBL: AF129113; AAD26364.1; -
DR InterPro: IPR002110; -
DR InterPro: IPR002111; -
DR Pfam: PF00023; ank; 3.
DR PROSITE: PSS0088; ANK_REPEAT; 1.
DR PROSITE: PSS0297; ANK_REPEAT_REGION; 1.
DR SMART: SM00248; ANK; 1.
DR Receptor.
SQ SEQUENCE 761 AA; 86689 MW; 46A281183EB672F CRC64;

Query Match 76.2%; Score 3051.5; DB 11; Length 761;
Best Local Similarity 77.7%; Pred. No. 2.2e-222;
Matches 598; Conservative 62; Mismatches 93; Indels 17; Gaps 7;

QY 1 MTSSSSPVFLFETLDGQEDGSEADGKLDPGSGLPMEQFQGEDRKFPQIRVNLNY 60
DB 1 MTSASNPAPFLFETSDGDEGSAEVNKGKQF---PPMESPFQGEDRNFSPOIKVNLNY 56
QY 61 ---RKGTA-SQDPNFRDRDLFNAVSRGVPEDLAIPYLSTKSKYLTDESEYEGST 115
DB 57 IKRPPKNTSAPSOQEPDRFRDRLEFVSRCVPEELTGLEYLRNRSKYLTDSAYTEGST 116
QY 116 KGTCLMKRVNLKQGVNACILPLQIDRDSGNPQPLVNAOCTDDYRGSHALHIAIEKRS 175
DB 117 KGTCLMKRVNLKQGVNACILPLQIDRDSGNPQPLVNAOCTDEYRGSHALHIAIEKRS 176
QY 176 LQCVKLAVENGANVHARACGRPFQKQGTCEYFGEPLSLAACKTQMDVSYLLENPHOP 235
DB 177 LQCVKLAVENGANVHARACGRPFQKQGTCEYFGEPLSLAACKTQMDVSYLLENPHOP 236
QY 236 ASLOATDSQGNVTHALVMIISDNSAENIALVTSMDGLQAGARLCPVQLEDIRNLQD 295
DB 237 ASLEATDSIGNVTHALVMIADNSPENSALVIMYDSLLQMGARLCPVQLEDISNHQGL 296
QY 296 TPLKIAAEGKTEIFRHLQREFSGT-SHLSRKFTWCYGVAVRSLYDLASVDSCEENV 354
DB 297 TPLKIAAEGKTEIFRHLQREFSGT-SHLSRKFTWCYGVAVRSLYDLASVDSCEENV 356
QY 355 LEIIAFHCKSPHRRMVLEPLNKLQAKWDLIPKFLNFCNLVYMFTRAVAHOPITKQ 414
DB 357 LEIIAFHCKSPHRRMVLEPLNKLQAKWDLIPKFLNFCNLVYMFTRAVAHOPITKQ 416
QY 415 LKQOAPHLKAEGNSMLTGHLLILGILYLLVQGLWFMRRHVFIMISFIDSEIFELF 474
DB 417 LQOAPHLKAEGNSMLTGHLLILGILYLLVQGLWFMRRHVFIMISFIDSEIFELF 476
QY 475 LFOALLTVVSOVLCFLAIETWYLPPLVSALVGLWNLVYTRGFQHTGITSVMIOKVILRD 534
DB 477 LFOALLTVVSOVLCFLAIETWYLPPLVSALVGLWNLVYTRGFQHTGITSVMIOKVILRD 536

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QY 535 LRFLLIYVLFEGFVALVLSIQEAMREAPTPGNATESVQPMQEDGNGCAOYRGIL 594
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 537 LRFLLIYVLFEGFVALVLSIREARSPKAPEDNNSTVEQPTVQEEB--PAPRSIL 594
QY 595 EASLELKFPTIGGELAFQOLHFRGMVLLLLAYVLTITLLNMLIAMSTVSVAT 654
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 595 DASLELKFPTIGGELAFQOLHFRGMVLLLLAYVLTITLLNMLIAMSTVSVAT 654
QY 655 DSWSIKRLQKALSIVLEMENGYMWC-RKKORAGVMTLVGTRPDGSPDERMCFRVEEYNNAS 713
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 655 NSMSIKRLQKALSIVLEMENGYMWCRRKKHREGRLKVGTRGDSCTPDERMCFRVEEYNNMA 714
QY 714 WEQTLPTLCEBDSGAGVPTLENPVLASPPKEDDGASEBNYVPVOLLOS 763
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 715 WEKTLPTLSEDSGPGITGNKKNPT----SKPGKNSASEDHLPLOVLOS 760
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RESULT 5
ID 090YH8 PRELIMINARY: PRT: 761 AA.
AC 090YH8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE STRETCH ACTIVATED CHANNEL 2B.
GN RSAC2B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishibashi K.;
RT "Molecular cloning of a stretch activated channel from rat kidney.";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB029330; BAA8637.1; -.
DR InterPro; IPR002110; -.
DR Pfam; PF00023; ank. 3.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
DR SMART; SM00248; ANK. 1.
SQ SEQUENCE 761 AA; 86705 MW; 8977CDE1D5351EC8 CRC64;
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Query Match 76.0%; Score 3041.5; DB 11; Length 761;
Best Local Similarity 77.5%; Pred. No. 1.4e-231;
Matches 597; Conservative 62; Mismatches 94; Indels 17; Gaps 7;
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QY 1 MTSPPSSPVFRLETTLDGQEDGSEADRGKIDFGSGLPPEMSQFOGEDRRKFAQIRVNLNY 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTSASSPAPFRLSETSDGDEGNAEVNKGQOE---PPMESPFQREDRNSSPQIKVNLNF 56
QY 61 ----RKGTGA-SQPPNRRDRDLFNAVSRGVPEDLAGLPETLSKTSKLTSETTEGST 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 IKRPKNTPASQOEPRDRDLFNAVSRGVPEELTGLELVRNMSKTLTDSATYEGST 116
QY 116 GRTCLMKAVLNLDGYNACILPILQIDRDSGNFQPLVNAQCTDDYRGHSALHIAIEKRS 175
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 117 GRTCLMKAVLNLDGYNACIMPLQIDKDSGNPKLLVNAQCTDEFQGSALHIAIEKRS 176
QY 176 LQCVKLLVNGANVHARACGREFQKGQGTCTFYFGEELPLSLAACKTQMDVYVYLLENPHQ 235
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 LQCVKLLVNGADVHLRACGREFQKHQGTCTFYFGEELPLSLAACKTQMDVYVYLLENPHQ 236
QY 236 ASLQATDSQGNVYLAHVNMSNSANIALVMSMYGILLQAGARLCPTVQLEDIRNLQDL 295
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 237 ASLQATDSQGNVYLAHVNMSNSANIALVMSMYGILLQAGARLCPTVQLEDIRNLQDL 296
QY 296 TPLKTLAAKSGKLEIFRHIIQORESG--LSHLRKFTEMCYGPVNSLYLDASVDSCEENSV 354
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 297 TPLKTLAAKSGKLEIFRHIIQORESGPYPLSKRFTMCYGPVNSLYLDASVDSCEENSV 356
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QY 355 LETIAHCKSPRRHRNVLEPLNKLQAKMDLLIPREFNLNLIYMEIFAVAYHQP 414
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 357 LETIAHCKSPRRHRNVLEPLNKLQEKMDRLVSRFFEFACYLVMYFTVAVYHQP 416
QY 415 LKQAPPHLKAPEGNMGLTGLTLLGGYLLVGLQWFMWRHVRPIMTSDSYEELF 474
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 417 LQDPALPSSKATFGESEMLLGLTLLGGYLLVGLQWFMWRRLPIMTSDSYEELF 476
QY 475 LFGALLTVASQVLCFLAIEWYLPLEVSATVLGWLNLVYTRGPHGTISVMIOKYLND 534
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 477 LQALLTVLSQVLRFEETEMVLPVLVLSVLGWLNLVYTRGPHGTISVMIOKYLND 536
QY 535 LRFLLIYVLFEGFVALVLSIQEAMREAPTPGNATESVQPMQEDGNGCAOYRGIL 594
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 537 LRFLLIYVLFEGFVALVLSIREARSPKAPEDNNSTVEQPTVQEEB--PAPRSIL 594
QY 595 EASLELKFPTIGGELAFQOLHFRGMVLLLLAYVLTITLLNMLIAMSTVSVAT 654
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 595 DASLELKFPTIGGELAFQOLHFRGMVLLLLAYVLTITLLNMLIAMSTVSVAT 654
QY 655 DSWSIKRLQKALSIVLEMENGYMWC-RKKORAGVMTLVGTRPDGSPDERMCFRVEEYNNAS 713
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 655 NSMSIKRLQKALSIVLEMENGYMWCRRKKHREGRLKVGTRGDSCTPDERMCFRVEEYNNMA 714
QY 714 WEQTLPTLCEBDSGAGVPTLENPVLASPPKEDDGASEBNYVPVOLLOS 763
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 715 WEKTLPTLSEDSGPGITGNKKNPT----SKPGKNSASEDHLPLOVLOS 760
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RESULT 6
ID 09JMI8 PRELIMINARY: PRT: 762 AA.
AC 09JMI8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ION CHANNEL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki M.;
RT "Ion channel.";
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB022332; BAA93435.1; -.
DR InterPro; IPR002110; -.
DR Pfam; PF00023; ank. 3.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
DR SMART; SM00248; ANK. 1.
SQ SEQUENCE 762 AA; 86767 MW; CE0970BC4193531E CRC64;
```

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Query Match 75.6%; Score 3028.5; DB 11; Length 762;
Best Local Similarity 77.4%; Pred. No. 1.5e-230;
Matches 594; Conservative 62; Mismatches 94; Indels 17; Gaps 7;
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```
QY 1 MTSPPSSPVFRLETTLDGQEDGSEADRGKIDFGSGLPPEMSQFOGEDRRKFAQIRVNLNY 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTSASSPAPFRLSETSDGDEGNAEVNKGQOE---PPMESPFQREDRNSSPQIKVNLNF 56
QY 61 ----RKGTGA-SQPPNRRDRDLFNAVSRGVPEDLAGLPETLSKTSKLTSETTEGST 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 IKRPKNTPASQOEPRDRDLFNAVSRGVPEELTGLELVRNMSKTLTDSATYEGST 116
QY 116 GRTCLMKAVLNLDGYNACILPILQIDRDSGNFQPLVNAQCTDDYRGHSALHIAIEKRS 175
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 117 GRTCLMKAVLNLDGYNACIMPLQIDKDSGNPKLLVNAQCTDEFQGSALHIAIEKRS 176
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Qy 176 LQCVLTVENGANVHARACGRFFQKGCCTCYFGEPLPLSLAACKQMDVSVLLENPHOP 235
    |||||
Db 177 LQCVLTVENGANVHARACGRFFQKGCCTCYFGEPLPLSLAACKQMDVSVLLENPHOP 236
Qy 236 ASLQATDSOGNTVTHALVMSIDNSAENALATVSMYDGLQAGARICPTVQLEDIRNLQDL 295
    |||||
Db 237 ASLEATDSLQNTVTHALVMSIDNSAENALATVSMYDGLQAGARICPTVQLEDIRNLQDL 296
Qy 296 TPLKLAKEGKIEIFRHLQREFSG-LSLHRSKFTEMCYGPRVSLYDLASVDSCEENSV 354
    |||||
Db 297 TPLKLAKEGKIEIFRHLQREFSGPQPLSKRFTEMCYGPRVSLYDLASVDSCEENSV 356
Qy 355 LEITAFHCKSPRRHRRMVLEPLNKLQAKMDLLPKFFLNLCLNTYMFITPAAYHQP 414
    |||||
Db 357 LEITAFHCKSPRRHRRMVLEPLNKLQAKMDLLPKFFLNLCLNTYMFITPAAYHQP 416
Qy 415 LKQAPLPLKAEVGNMMLTGHIILGLGIVLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV 474
    |||||
Db 417 LDQPAIPSSKATFGESMILLGHILLGLGIVLVGLVGLVGLVGLVGLVGLVGLVGLVGLV 476
Qy 475 LFOALLTVSOVLCPLAEMVLEPLVSLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV 534
    |||||
Db 477 LQQALLTVSOVLCPLAEMVLEPLVSLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV 536
Qy 535 LLRFLILVLEPLFGPAVALVLSLOEAMRPEAPTPGNATESVOPMEGODEGNAQYRGL 594
    |||||
Db 537 LLRFLILVLEPLFGPAVALVLSLOEAMRPEAPTPGNATESVOPMEGODEGNAQYRGL 594
Qy 595 EASLELFFETIGMGLAEOBOLHFRGMVLLLLAVLLVLLVLLVLLVLLVLLVLLVLLVLLV 654
    |||||
Db 595 DASLELFFETIGMGLAEOBOLHFRGMVLLLLAVLLVLLVLLVLLVLLVLLVLLVLLVLLV 654
Qy 655 DSWSMWLQKAIISYLEMENGWYWC-RKQKAGVMLTVGTPKSPDERMCFEVEENNAAS 713
    |||||
Db 655 NSMSIMWLQKAIISYLEMENGWYWC-RKQKAGVMLTVGTPKSPDERMCFEVEENNAAS 714
Qy 714 WEQIPLTLCEDPSGAGVPTLENPVLSPPKEDDGASEENVVQOLQ 760
    |||||
Db 715 WEQIPLTLCEDPSGAGVPTLENPVLSPPKEDDGASEENVVQOLQ 757
RESULT 7
035433 PRELIMINARY; PRT; 838 AA.
AC 035433;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE VANILLOID RECEPTOR SUBTYPE 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96007969; PubMed=9349813;
RA Caterina M.J., Schumacher M.A., Tomlinaga M., Rosen T.A., Levine J.D.,
RT Julius D.;
RT "The capsaicin receptor: a heat-activated ion channel in the pain
    pathway".
RL Nature 389:816-824(1997).
DR EMBL; AF029310; AAC53398.1; -.
DR InterPro; IPR002110; -.
DR InterPro; IPR002111; -.
DR Pfam; PF00023; ank. 3.
DR PROSITE; PS50088; ANK_REPEAT. 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION. 1.
DR SMART; SM00248; ANK. 1.
SQ SEQUENCE 838 AA; 94947 MW; DAFCC80B12BDF71BF CRC64;
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Matches 359; Conservative 127; Mismatches 230; Indels 60; Gaps 15;
Qy 18 GOEDSEADRGKLDGSGSLPPMESQFOGEDRRKFAPIRVN---LNYRKGTCG----- 65
    |||
Db 51 GKGOSEAS-----PLDCPEEGGLASCPILIVSSVLTIGRGDDPASPVRSSQ 99
Qy 66 ----ASQDPNRFDRDLFMAVSRGVPEDLAGLEPYLSKTSKYLTDSYTGSGTGKTCM 121
    |||
Db 100 DVSAGKRPRLYDRRSIFDVAQSNCOELSLPLFLORSKKRLDSSEFKPPEKTCCL 159
Qy 122 KAVINLKQGVNACILPLQIDRDGSGNPQVYNAQCTDIDYGHGSHAIKRSLOQCKL 181
    |||||
Db 160 KAVINLKQGVNADITALLDLVAKTKDSLQFVNASTDSYTGQALHAIKRSLOQCKL 219
Qy 182 LVENGANVHARACGRFFQKGCCTCYFGEPLPLSLAACKQMDVSVLLENPHOPASLOA 240
    |||||
Db 220 LVENGANADVQAANAGOFFKKTGRPGFYGELPLSLAACKQMDVSVLLENPHOPADISA 279
Qy 241 TDSQNTVTHALVMSIDNSAENALATVSMYDGLQAGARICPTVQLEDIRNLQDLTPLK 300
    |||||
Db 280 RDSVGNFVTHALVEVADVTNTEKVTSMYNEILLGAKLHPTLKEITNRKGLTPLAL 339
Qy 301 AAKBKIEIFRHLQREFSG-LSLHRSKFTEMCYGPRVSLYDLASVDSCEENSVLEI 358
    |||||
Db 340 AASSGKIGVLLVLELHEPBCRLSKFTEMAGPVHSSLYDSCIDTEKNSLVEI 399
Qy 359 AF-HCKSPRRHRRMVLEPLNKLQAKMDLLPK-FPLNFCNLVLMFTPAAYHQP 416
    |||
Db 400 AYSSEFTNRRHMDLVEPLNKLQAKMDLLPKFIFNFVYCLMIFTAAYRVP-- 457
Qy 417 KQAPD-HLKAEGVNSMLTGHIILGLGIVLVGLVGLVGLVGLVGLVGLVGLVGLVGLV 474
    |||
Db 458 -EGLPYKIKMTVGVGFVTEGELLVSGGVYFFFGCIYFLQRRSLKSLFVDSYEILF 516
Qy 475 LFOALLTVSOVLCPLAEMVLEPLVSLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV 534
    |||
Db 517 FVQSEMLVSVLVLFQSRKEVVASVFLAMGWIMLVLTGFGFQMGYAVVIMELI 576
Qy 535 LLRFLILVLEPLFGPAVALVLSLOEAMRPEAPTPGNATESVOPMEGODEGNA----- 588
    |||
Db 577 LCREFEVVLEPLFGSTAVVLIED-----GN---NSLPMSTPHKRGSKACRGN 625
Qy 589 QYRGILEASLELFFETIGMGLAEOBOLHFRGMVLLLLAVLLVLLVLLVLLVLLVLLVLLV 648
    |||
Db 626 SYNLSYSTLELFFETIGMGLAEOBOLHFRGMVLLLLAVLLVLLVLLVLLVLLVLLVLLV 685
Qy 649 VNSVATDSMSIMWLQKAIISYLEMENGWYWC-RKQKAGVMLTVGTPKSPDERMCFEVE 707
    |||
Db 686 VNKLQESKNIMWLQKAIISYLEMENGWYWC-RKQKAGVMLTVGTPKSPDERMCFEVE 745
Qy 708 EVNNASMEQTLPTLCEDPSGA-GVPTLENPVLSPPKEDDGASEENVVQOLQ 762
    |||
Db 746 EVNNATVNTVNGIINEDRGNGCVARTISFLRS-----RVSGRWKMFALVPLLR 797
RESULT 8
09JMS7 PRELIMINARY; PRT; 838 AA.
ID 09JMS7;
AC 09JMS7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE VANILLOID RECEPTOR TYPE 1 LIKE PROTEIN 1.
GN VRIL1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Tsutsumi S., Nakamura A., Kohama K.;
RT "Vanilloid receptor type 1 like protein 1.";
RT Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
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DR EMBL: AB040873; BAA94307.1; -
 DR InterPro: IPR002110; -
 DR InterPro: IPR002111; -
 DR Pfam: PF00023; ank; 3.
 DR PROSITE: PS00086; ANK_REPEAT; 1.
 DR PROSITE: PS02097; ANK_REPEAT_REGION; 1.
 DR SMART: SM00248; ANK; 1.
 DR Receptor.
 SQ SEQUENCE 838 AA; 94964 MW; EE33CEAA606C3404 CRC64;

Query Match 41.3%; Score 1652; DB 11; Length 838;
 Best Local Similarity 46.3%; Pred. No. 8e-122;
 Matches 359; Conservative 127; Mismatches 230; Indels 60; Gaps 15;

QY 18 GQDSEADGKIDFGSGLPMSQFQGEDRKAPQIRVN---LNRKKG--- 65
 DB 51 GKGDSEAS-----PDDCPYEEGLASCPITVSSVLTQRPDGPASVRSQ 99
 QY 66 ---ASQPDNRPDRDLFMAVSRGVPEDLAGPEYLSTKSKYLTDESEYEGTKTCLM 121
 DB 100 DVSAGEKPPRLYDRSIFPAVANSQCELESLLPFLQSKKLTDSFQDPETGKTCLL 159
 QY 122 KAVLNLDGVNACTLPDLQIDRSGNPQLVNAQCTDDYRGHSALHAIERKSLOCVKL 181
 DB 160 KAMLNJHNGQNTITALLDVARKDSLKFVNASVYDTSYKGGTALHAIERNMTLVTL 219
 QY 182 LVNGANVHARACGRFFQKQGG-TCFYFGLPLSLACTQMDVSYLLENPHQPSLOA 240
 DB 220 LVNGADVQAAANGDFPKKRGPFEGELPLSLAQTQALIVFELQNSQPADISA 279
 QY 241 TDSQGVTLHALVMSIDNSAENIALVTSMDGLQAGARLCPVQLEDINLQDLPPLKL 300
 DB 280 RDSVGVTLHALVEADVNDTNDTKFTSMKNELLIGAKHPLKLEITNRKGLPPLAL 339
 QY 301 AAKGKIEIFRHLQREF--SGLSHLSRKFTWCYGRVSLYDLASVDSCEENSVLEIT 358
 DB 340 AASSGKIGVLAAYILOREIHEPCCRHLRSKFTENAYGVSHSLYDSCIDCEKNSVLEVI 399
 QY 359 AF-HCKSPHRRVAVLEPLNKLLOAKMDLLIPK-FELNFCNLIMYFIETFAVAYHOPTLK 416
 DB 400 AVSSSETPNRHDMLVLEPLRLLODKMDRFVKRIFFNFVYCLYMLITFAAAYRPV-- 457
 QY 417 KOAP--HKAEGVNSMLTGHILLGLGYLLVQOLWFMRRHVFIMLSFIDSEIIF 474
 DB 458 -EGLPPYKLTNTVGDYFRVYTGELISVSGVYFPFRGIQYLRPSKLSFVDSYSLIF 516
 QY 475 LFOALLTVVSQVLCFLAIEYVLPVLSALVGLNLTYYRGQHTGHSVMIQKYLKD 534
 DB 517 FVQSLFMLVSVVLYFQORKEYVASWFSIAMGWTNMLYTRGFQOMGIYAVMIETKMLRD 576
 QY 535 LRFELIYVLEFGFVALVLSLSQEMARPEAPGPNATESVOPMEQDEGNGA----- 588
 DB 577 LCFMRYVYVLEFGFSTAVVTLIED-----GKN---NSLPMESTPHKCRSACKPGN 635
 QY 589 QYRGILEASLELFTKIGMELAFQOLHFRGMVLLLLAVLYLTYLLNMLIALMSET 648
 DB 626 SYNSLSTGCTELKFTIGMDLEFENYDKAVFIILLAVLYLTYLLNMLIALMGET 685
 QY 649 VNSVAIDSMISIMKLOKALISVLEMGYWMW-RRKQRAQVMTLVGTGPDGSPDERKCPRE 707
 DB 686 VNKIAESKIMVLOKALITLDEKSFLLCMKRAFRSGKLQVFPDGDVDMWCFRVD 745
 QY 708 EVNWMASMEQTLPTLCEPDSGA-GVPRTLENPVLASPKEDDEGASEENVYVQOLQ 762
 DB 746 EVNMTTWNINVGIIINEDPGNCEGVKRTLSFLSKSG---RVSGRMKNKFAVPLLR 797

RESULT 9
 ID 09H304 PRELIMINARY: PRT; 839 AA.
 AC 09H304;
 DT 01-MAR-2001 (TREMBLrel, 16, Created)

DT 01-MAR-2001 (TREMBLrel, 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel, 16, Last annotation update)
 DE CAPSACIN RECEPTOR.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cortright D.N., Peck A., Zou T.;
 RT "Cloning and characterization of the human capsacin receptor, VR1.";
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF196175; AAG43466.1; -
 DR Receptor.
 SQ SEQUENCE 839 AA; 94968 MW; EA9BF7D6023EF9F4 CRC64;

Query Match 41.2%; Score 1651.5; DB 4; Length 839;
 Best Local Similarity 48.5%; Pred. No. 8e-122;
 Matches 344; Conservative 122; Mismatches 199; Indels 45; Gaps 11;

QY 74 FDDRLFNARVSRGVPEDLAGPEYLSTKSKYLTDESEYEGTKTCLMRAVLMKQGVNA 133
 DB 113 YDRRSIFEAVAQNNCODLESLLFLQKSKHLTDNEFKDPEKTEKTLKAMLMHGGQNT 172
 QY 134 CILPLQIDRDSGNPQPLVNAQCTDDYRGHSALHAIERKSLOCVKLIVNGANVHARA 193
 DB 173 TIFLLEIARQDTSIKELVNASTDYIKQIHLHAIERNALVTLVENGADVQAAA 232
 QY 194 CGRFQKQGG-TCFYFGLPLSLACTQMDVSYLLENPHQPSLOADDSQNTVLAHL 252
 DB 233 HGDFPKKTRGPRGYFGEGLPLSLAQTQALIVFELQNSQPADISARDSVPTVLAHL 292
 QY 253 VMISDMSAENIALVTSMDGLQAGARLCPVQLEDINLQDLPPLKLAKEKIEIFRH 312
 DB 293 VEADVNTAONTKFTVSMYEMILMLGAKLHPTLKLELTNNKGMTPLALAGTGKIVLAV 352
 QY 313 ILQREFS--GLSHLSRKFTWCYGRVSLYDLASVDSCEENSVLEITAF-HCKSPHRR 369
 DB 353 ILQRELOEPCRLSLSKFTFMAAGVSHSLYDSCIDCEKNSVLEVIYVSSSETPNRHD 412
 QY 370 MVVLEPLNKLLOAKMDLLIPK-FELNFCNLIMYFIETFAVAYHOPTLKQAPDHLKAE-V 427
 DB 413 MLVLEPLNRLLODKMDRFVKRIFFNFVYCLYMLITFAAAYRPV---DGLPPFMEXI 469
 QY 428 GNSMLTGHILLGLGYLLVQOLWFMRRHVFIMLSFIDSEIIFLFOALLTVVSQV 487
 DB 470 GDFRYVTGELISVSGVYFPFRGIQYLRPSKLTSEMLEFLOSLPMLATVYL 529
 QY 488 CFLAIEMYVLPVLSAVLGLNLTYYRGQHTGHSVMIQKYLRLFLIYVLPFL 547
 DB 530 YFHLKAEYASWFSIALGWTNMLYTRGFQOMGIYAVMIETKMLLDLCRFMRYVLPFL 589
 QY 548 GFPAVLVLSQEA-----WRBPAPGPNATESVOPMEQDEGNGAQRGLI 594
 DB 590 GFSTAVVTLIEDKNDLSESTSHRWGPACRPDSS-----YNSLY 632
 QY 595 EASLELFTKIGMELAFQOLHFRGMVLLLLAVLYLTYLLNMLIALMSETVSVAF 654
 DB 633 STCELELFTKIGMELAFQOLHFRGMVLLLLAVLYLTYLLNMLIALMGETVVKIAQ 692
 QY 655 DWSIMKLOKALISVLEMGYWMW-RRKQRAQVMTLVGTGPDGSPDERKCPREYEVNMA 713
 DB 693 ESKNIMKLOKALITLDEKSFLLCMKRAFRSGKLQVYTPDGKDDYRMCFRDEVNMT 752
 QY 714 WQOTLPTLCEPDSGA-GVPRTLENPVLASPKEDDEGASEENVYVQOLQ 762
 DB 753 WNTNVIINEDPGNCEGVKRTLSFLSKSG---RVSGRMKNKFAVPLLR 798

RESULT 10
 ID 09H09 PRELIMINARY: PRT; 839 AA.
 AC 09H09;
 DT 09H09

AC Q9H0G9: 2001 (Tremblrel, 16, Created)
 DT 01-MAR-2001 (Tremblrel, 16, last sequence update)
 DT 01-MAR-2001 (Tremblrel, 16, last annotation update)
 DE HYPOTHEICAL, 94.9 KDA PROTEIN.
 GN Dkf2p434k0220.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Ostersmaelder B., Ostersmaelder B., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL136801; CAB66735.1; -.
 KW Hypothetical protein.
 QO SEQUENCE 839 AA; 94950 MW; EA9BF7D603AE4760 CRC64;

Query Match	41.2%	Score 1648.5	DB 4	length 839
Best Local Similarity	48.5%	Prod. No. 1.5e-121		
Matches 344	Conservative 122	Mismatches 199	Indels 45	Gaps 11

QY 74 FDRRLFNVAARGVEDIAGLEPEYLSKTSKLTDESEYSGSKYKMLKAVNLKDVNA 133
Db 113 YDRSRIFEFAVANNQODLESILLFLQSKKHILTDNEFDPEGRKCTCLKAMLNHDCQNT 172
QY 134 CILPLLOIDRDSGNPOPLVNAQCTDDYIRGSHALIAIEKSLQCYKLVENGAVNHARA 193
Db 173 TIFPLELEIAROTDSLKELELVNASTYDSYKQGTALHIAIEERRMALVYTLVLENGAVNAAA 232
QY 194 GCRFFOKQSG--TCFEGELPLSLACTKOWDVSVLLEPNHPQASTOATDSQGNVTAL 252
Db 223 HGDFPKKTKRGPRGFEGLSPSLACTQOLGKVKLLQNSMOTADISARDSGNTVIAL 292
QY 253 VMISDSENALIALVTSMDGLLOAGARCLPTVOLEDIRNLQDLPYLKLAKEGKIEIFRH 312
Db 293 VEVDNFTADNKRKFVTSMTNELILIGAKLHPPLKEELTNKKKMPLEALAAAGKIGVLA 352
QY 313 ILOREFS--GUSHSRKTECMQGVARSIVXDASVSDCEENSVLEITAF--HCKSPHNR 369
Db 353 ILQRIQIEBCHRSKRKTEEMAGCGVHSSLDSCIDCEKSVLEVLAIVSSSETPNRHD 412
QY 370 MVVLEPLKLLOAKMDLLIPK--FEPNFCNLIMYEIFFAVAYHOPELTKKOAPHKAE--V 427
Db 413 MLVLEPLRLRLQDKMDRVRVKRIFENFLVYCYLMIIFMAAYRRV---DGLPRPKMEKI 469
QY 428 GNSMLITGHIIILLAGIYLLVGQLYEMRHRVFIWISTIDSEFILLPLFOALLVVSQVL 487
Db 470 GDYFVWGTIELSVLGGVYFEPFGIOYFLQRRPSMKTLFVDSYSEMLFLOSILMATAVL 529
QY 488 CFLATEWYLLVLSALVGLNLELYYRGPFOHTGYTSWIOKVIIRDLRFLIYLVLF 547
Db 530 YFSHKEVYASNVSLALGNTMLYTTGFOOMGIYAAIMEKMLLRDLCREHFVYIVLEF 589
QY 548 GFAVALVLSQEA-----WRPEAPGTGNATESVOPMGQDEGNGAORYGL 594
Db 590 GFSTAVYVLLIEDGKNDSLPESTSHRMGAPCARPDSS-----YNSLY 632
QY 595 EASLELFEFTGMGLAQOBOLHFRGMVLLILLAVLTYLILMLTALMSEYVNSAT 654
Db 633 STCELEFETTGMOGLETEYNDFAVYTLILLAVILTYLILMLTALMGEYVNTKIAQ 692
QY 655 DSWSIWKLQAKAISVLEMGYVMC--RKQORAGVMILVTGKPDGSPDEMRCCFVEEYNAS 713
Db 693 ESKNIMKLQRAITITIDTEKSFCLKMRKAFRSGKILLQVGYTPDGKXDYHMCPRVDEVNNT 752
QY 714 WEOTLPLTLCEDPSGA--GYPRILENDVSLAPKREDEGASSENYVAVOLLO 762
Db 753 WNTVANGIINDEPGNCEGVKRLTSPLSRSL---RVSGHMKMNAVALPPLR 798

RESULT	11			
Q9NQ74				
ID	Q9NQ74	PRELIMINARY:	PRT:	839 AA.
AC	Q9NQ74;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	VANILLOID RECEPTOR 1.			
GN	VAR1.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Ketseil R.E.;			
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Hayes P., Meadows H.J., Harries M.H., Duckworth M.D., Cairns W.,			
RA	Harrison D.C., Clarke C., Gunthorpe M., Ellington K., Prinjha R.K.,			
RA	Barton A.J., Medhurst A.D., Smith G.D., Topp S., Muddock P.,			
RA	Sanger G.J., Terrett J.B., Jenkins O., Randall A., Benham C.D.,			
RA	Gloger I.S., Davis J.B.;			
RT	"Cloning and functional expression of a human orthologue of rat			
RT	vanilloid receptor-1.";			
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AJ277028; CAB95729.1; -.			
DR	InterPro: IPR002110; -.			
DR	InterPro: IPR002111; -.			
DR	Pfam: PF00023; ank. 3.			
DR	PROSITE: PSS0088; ANK_REPEAT. 1.			
DR	PROSITE: PSS0297; ANK_REPEAT_REGION. 1.			
DR	SMART: SM00248; ANK. 1.			
KW	Receptor.			
SEQUENCE	839 AA; 94923 MW; 7142FFAE43189ECC CRC64;			

Query Match	41.1%	Score 1644.5	DB 4	Length 839
Best Local Similarity	48.5%	Pred. No. 3.1e-121		
Matches 344	Conservative 121	Mismatches 200	Indels 45	Gaps 11

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OY 74 FDRORLNAVRGVPEDLAGPELSTKSTKLTQSEYEGSTGTCMLKAVLNLDG VNA 133
Db 113 YDRSRIFEAVAAQNNCODESLLEFLQKSKKHLTDNEFDEPDTGTCCLKAMLNHDGONT 172
OY 134 CILPELOIDRDSGNPQPLVNAQCTDDYVYRGSHALHIAIEKRSLOCVKLLVENGANVHARA 193
Db 173 TILPELEIARQDLSKELVNASYDSYKCGQALHIAIERNNMALVTLLVENGADVQAA 232
OY 194 CGRFQKQGC -TCYFPEGLPLSLAACKTQMNVSYLLENPHQPSLQATTDGQGMVJHAL 252
Db 233 HGDFPFKTKGPGFYEGELPLSLAACKTQGLIYVFLQNSMOTDISKSDSVGNVTJHAL 292
OY 253 VMISDSEANIALVTSMWDGLQAGARLCPTVOLEDJEDJLNMODLPLKAAKEKTEIFRH 312
Db 293 VEVADNADNKKFTYSMTNELLIIGAKHLPLKLEELTNKKGMPIPLMAAGTGIVLAY 352
OY 313 ILOREFS- -GISHLSRKFTKCYGPRVRSYLDLASVDSCEBNSVLEITAF- HCKSPHRHR 369
Db 353 ILOREIOBPBECRHLSRKFTTEWAYSGPVHSLYDLDCIPDCEKNSVLEIYVSSSETPNRHD 412
OY 370 MMYLEPILNKLLQAAKWDLLIPK-FFLNFCLNLIWFIFFAVAYHOPPTLKKQAAPLKA- V 427
Db 413 MLALVEPRLQDDQMDWRKVRKRIFFNFNLVYCLYMIIFMAAYTRV-- -DGLPPFKMEKT 469
OY 428 GNSMLTGHLLILGCIYLLVQGLMAYFWRHRVFWISFIDSYFEILFLFOALLTVVSQVL 487
Db 470 GDYPRVYGEILSYLVGYVFFFRGIOYFLQRRPSKLTFLVDSSEMLPEFLOSLFWLATAVVL 529
OY 488 CFELAIEWYLLPLVASLVGLMNLVYTRRGQHTGIVSYMIOKTVLLRDLRLLLVYVFLF 547
Db 530 YFSHUKYVASWFSLALGWTNMLYTRRGQDMQIVAVVAMEKMLLRDLRCRFMFYVYVFLF 589

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[illegible][illegible]


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Db 157 SFLTHKRRLDDEERESTGKTCIPKALLNLSAGRNDTIPILDIAEKTGMREFINSP 216
Qy 156 CTDYYRGHSALHIAIEKRSLOQVLLVNGANGANNHARACGRFO-KGOGTCFFEGELPLS 214
Db 217 FRDYYRGQATLHIAIERCKHYVELLVEKGDADVAQARGFORCKDEGGYVFEGLPLS 276
Qy 215 LAACRKQMDVSYLLENHOPASLOATDSOGNTVLAHVMISDNSENALVTSYDGL 274
Db 277 LAACNQHPIVHYLENHOKQADLRQDSRGNTVLAHVALADNRENTKFTVMYDGL 336
Qy 275 OAGARLCPTVOEDIRNLODLPKLAKKEGTEIFRHILOREFS--GISHSRKFTEMC 332
Db 337 IKCAKLPEDTNIEALLNDGSLPLMAAKTGKIGTFQHIIRRELDDEDEVRHLRSFKDMA 396
Qy 333 YGPRVSYLDLASVDSG--EENSVELEIIAFHCKSPHRHBMVLEPLKLQAKWDL-IPK 390
Db 397 YGPRVSYLDLSIDTCGEVSVLEIIVYNSKIEHRHMLAVERINELLRDKWRKFGAVS 456
Qy 391 FFLNFLCNLIYMTFTTAVAYHOPTLKQOAPHLKAEGNSMLTGHILLLGGIYLLVGQ 450
Db 457 FYISVSVYLCAMITFTLLAYYRP--MEGPPPYPTTIDYLRALAGEITLLTGLIFFESN 514
Qy 451 LWRVRRHVFPIWISFIDSYFELLFLFQALLTVYSQVLCFLAIEYRLPLVSALVGMN 509
Db 515 IKDLFMKRCPOVNSFEIDGSFOLLFYISVLYTAGLYGGEVAYLAVMFALVGMN 574
Qy 510 LLYYRGFOHTGIYSVMIOKYLRLDLRLIYVLFGLFAVALVSL-----SQE 559
Db 575 ALYFRGKLKLTGYSIMOKILFKDLFRLLVYLLFMIGVSALVSLNPPCSSSCSED 634
Qy 560 AMRPAAPPGPNATESVOPMEGOEDGNGAORYGLILEASLELFTTIGMELAFQOLHR 619
Db 635 HSNCTLPYPCRSODS-----QTFSTFLDLFKLTIGMDLEMLSAKYP 678
Qy 630 GMLVLLLAAYLLIYLLNMLIALMSETVNSVATDSIMKLOAIVLEMEHY-WMC 678
Db 679 GVFILLVYIILFFVLLNMLIALMGETVGVSKSHIMQLQATVLLDIERSFPL 738
Qy 679 RKKORAGVMLTVGTGPDGSPDERMCFRVEEVWMAAMEOTLPTLCDPGAG----- 729
Db 739 RRAFSGEMVYVKGKTDGTPDRMCFRVDVWMSHMNOLGIISDPKSDIYYQYGFSH 798
Qy 730 -----VPRLENPVLAAPKED 746
Db 799 TVGRLRDRMSTVYVRYVE--LNKSCPTED 826

RESULT 14
Q9HBCO PRELIMINARY; PRT; 871 AA.
AC Q9HBCO;
DT 01-MAR-2001 (Tremblrel. 16, created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE OTRPCA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RENAL CORTEX;
RX PubMed=11025659;
RA Strothmann R., Harteneck C., Nunnenmacher K., Schultz G., Plant T.D.;
RT "OTRPC4, a nonselective cation channel that confers sensitivity to
RT extracellular osmolarity".
RL Nat. Cell Biol. 2:695-702(2000).
DR EMBL; AF258465; AAG16127.1;
SQ SEQUENCE 871 AA; 98294 MM; C62056B86DEA6FB6 CRC64;

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Matches 339; Conservative 114; Mismatches 246; Indels 88; Gaps 16;
Qy 8 PVFRLTELDGGOEDS-----SEADRCK-LDFSGSLRPMESOFQGEDRKRAP----- 52
Db 32 PLSSLANLFEFG-EDGSLSPRADASRPAGDGRNLMMKRGQAVRKVPIDLESTL 90
Qy 53 -----QIRVNLNRYK-----GTGASQDP--NRFD 75
Db 91 YESSVVPKPKAMPDLSLDYGYTRHSSDNKRWKRIIEKOPQSPKAPAPPPILKVFN 150
Qy 76 RDLRFNAVSRGPEDLAIPREYLSKTYLTDSEXTGCTGKMLKAVNLKQDVNCCI 135
Db 151 RLPIEDIVSRGSTADLDGLPLPLTHKRRLDDEERESTGKTCIPKALLNLSGRNDTPI 210
Qy 136 LPLQIDIDSGNPOLVNAOCTDYYRGHSALHIAIEKRSLOQVLLVNGANGANNHARACG 195
Db 211 PYLLDIAERTGMREFINSPFRDIYRGQATLHIAIERCKHYVELLVAQGDADVAQARG 270
Qy 196 RRFQ-KGOGTCFFEGELPLSLAECTQMDVSYLLENHOPASLOATDSOGNTVLAHVM 254
Db 271 RFFQPKDEGGYVFEGLPLSLAECTQMDVSYLLENHOPASLOATDSOGNTVLAHVA 330
Qy 255 ISDNAENIALVTSYDGLQAGARLCPTVOEDIRNLODLPKLAKKEGTEIFRHIL 314
Db 331 IADNRENTKFTVMYDGLLILKCARLPFDSNLEAVLNNDGSLPLMAAKTGKIGTFQHI 390
Qy 315 QREFS--GLSHLSRKFTEMCYGPVRSYLDLASVDSG--EENSVELEIIAFHCKSPHRHNV 371
Db 391 RREVDEDTNRHLSRKFQMAVGYSSLYDLSIDTCGEASVLEIIVYNSKIEHRHML 450
Qy 372 VLEPINKLLQAKWDL-IPKFFLNFLCNLIYMTFTTAVAYHOPTLKQOAPHLKAEGNS 430
Db 451 AVEPINELLRDKWRKFGAVSEYINVSVCAMVITFLAYYQPL--EGTPPYPTTVDY 508
Qy 431 MLTGHILLLGGIYLLVGQ-LYRRHVFPIWISFIDSYFELLFLFQALLTVYSQVLCF 489
Db 509 LRLAGEVITLFGVLEFFNTIKDLFMKRCPOVNSFEIDGSFOLLFYISVLYSALVYL 568
Qy 490 LAIEYRLPLVSALVGMNLLYTRGFOHTGIYSVMIOKYLRLDLRLIYVLFGLF 549
Db 569 AGIEYRLAVMFAVLYLGMNMLYFRGLKLTGYSIMOKILFKDLFRLLVYLLFMIGY 628
Qy 550 AVALVSL-----SQEAMRPAAPPGPNATESVOPMEGOEDGNGAORYGLILEASLE 599
Db 629 ASALVSLNPPCSSSCSEDQNTCTVPTVPCRSODS-----EFSTFL--LD 672
Qy 600 LFKFTIGMELAFQOLHFRGNVLLLLAYLLIYLLNMLIALMSETVNSVATDSMSI 659
Db 673 LFKLTIGMDLEMLSTTRYPVVFIILVYIILFFVLLNMLIALMGETVGVSKSHI 732
Qy 660 WKLOKAISVLEMEHY-WMCKRKORAGVMLTVGTGPDGSPDERMCFRVEEVWMAAMEOTL 718
Db 733 WKLOKATITLIDERSFPLFKRAFSGEMVYVKGKSDGTPDRMCFRVDVWMSHMNOL 792
Qy 719 PTLCEDP 725
Db 793 GIINEDP 799

RESULT 15
Q9ER28 PRELIMINARY; PRT; 871 AA.
AC Q9ER28;
DT 01-MAR-2001 (Tremblrel. 16, created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE VANILLOID RECEPTOR-RELATED OSMOTICALLY ACTIVATED CHANNEL.
DE VROAC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

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Query Match 36.6%; Score 1467; DB 4; Length 871;
Best Local Similarity 43.1%; Pred. No. 3.4e-107;

RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RX PubMed-11081638;
RA Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RT Sali A., Hudspeeth A.J., Friedman J.M., Heiler S.,
RT "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
RL candidate vertebrate osmoreceptor.";
EMBL: AF263521; MAG28027.1; -
KW Receptor.
SQ SEQUENCE 871 AA; 98009 MW; 5D50684DA08C354B CRC64;

Query Match 36.6%; Score 1465.5; DB 11; Length 871;
Best Local Similarity 40.4%; Pred. No. 4.5e-107;
Matches 341; Conservative 128; Mismatches 257; Indels 119; Gaps 16;

QY 8 PYRRLTLDGGGDEDS-----EADRGKLDGSGLPMEGSGEDGRKFAF-----52
DB 32 PLSSLANLEGEGERSSSLSPVDASR--PAGPGDGRPMLRMKFGAFRKYVNPIDLESTL 90
QY 53 -----QIRVNLNRYRKGATGASQDPDPR-----FD 75
DB 91 YESSVYPGKKKAPMDLSFDYGTIRHHPSDKKRRKRYVEKQPOSKPAPAPQPPILKVFN 150
QY 76 RDRLEFNAVSRGVPEDLAGLPEYLSKTSKYLTDESEYEGSTGKTLKAVLNKQGVNACI 135
DB 151 RPIILFDIVSRGSPADLDGLSTYLLTHKKRLTDEFEPEPSTGKTLKALLNLSGRNDTI 210
QY 136 LPLLOIDRDSGNQPIVYNAOCTDYYRGSHALIAIEKRSLOCYKLLVENGANVHARAG 195
DB 211 PYLLDIAERTGNRKEPINSFRIYRGOTALHAIERCKHYVEILVAGADVAHQARG 270
QY 196 RFQO-KGQCTCFYFGEPLSLACTKOWDVSYLLENPHOPASLOATDSOGNTVLHALVA 254
DB 271 RFQOPDEGCFYFGEPLSLACTKOWDVSYLLENPHOPASLOATDSOGNTVLHALVA 330
QY 255 ISDNSAENIALVTSMDGLLQAGARLPTVQLEDIRNLQDLPELKLAKEGKIEFRHIL 314
DB 331 IADNTRENTKFEYKMYDLKLLKCSRLFPDSNLETVLINDGLSPLMAAKTGKIGVFOHII 390
QY 315 QREFS--GLSHLSKFTTEWCYGVRSYLDIASVDSG--EENSYLEIIFRCKSPHRRMY 371
DB 391 RREVTDEDTRHLSRKPKDMAYGPNVSSLDSCGEEVSYLEIVNYSKIEENHEML 450
QY 372 VLEPLKLLOAKMDLL-IPFEFLNFCNLTYMFIPTAVAYHOPTLKKQAPHLKAEVNS 430
DB 451 AVPEINELLROKRRKRGANSFYINVSYLCAMYIFTLAYOPL--EGTPPYRYRTTVDY 508
QY 431 MLTGHILLLGGIYLLVGLQW-YFWRRHVFYIWSFIDSYFEILLFEOALLTVVSOVLCE 489
DB 509 LRLAGEVITLLTGVLFFETSIKDLFMKCPGVNSLFVDSFQLLYFYISLVVVSAAVLY 568
QY 490 LAIEWLPLVLSALVYGLMLNLYYTRGFQHTGIYSVMIOKVIILRLRLIYLVLEGEF 549
DB 569 AGIEAVLAVVFAVLYGMMNALLYFTRGKLKLTGYYSIMQIKLEKDLFRFLVYLLFMIGY 628
QY 550 AVALVSL-----SOEAMRPEAPGTGNATESYQPMEGDEGNGAQYRGILLEASLE 599
DB 629 ASALVTLILNLPCTMKKACNEDQSNCTVSTPACDSS-----ETFSAFI--LD 672
QY 600 LPEFTIGMGELEAFQEOJLHFRGNVLLILLAYVLLTYILLNMLTALMSETVNSVATDSWSI 659
DB 673 LPELTLTGMGLDEMLSSAKYPVYVETILLVYIILTFVLLNMLALMGETYGVQSKESKHI 732
QY 660 WKLOKAIISYLEMENGY-AMCRKKQKQAGVMLJVGFKPDGSPDERWCFRVEEVNASKWEQTL 718
DB 733 WKLOMATTTILDIERSPVFLRKAFRSGEMVYVGSKSDGTPDRRMCFRVEDVNNSHNOML 792
QY 719 PTLCEPDS-----GAGVPRTELENPVILASPKDEDEGASEENVY 756
DB 793 GIINEDPGKSEIYQYIGFSHTMGLRLRRDRSSVYPRVVE-----LNKNSGTDEVVY 843

QY 757 PVQQL 761
DB 844 PLDNL 848

Search completed: July 18, 2001, 16:00:08
Job time: 136 sec

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